

Exhibit I

Query: SEQ ID NO: 7

BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (17 letters)

Results for: lcl|11866 None(17bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|11866

Description

None

Molecule type

nucleic acid

Query Length

17

Database Name

nr

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Distance tree of results](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Database

Posted date	Dec 28, 2008 5:47 PM
Number of letters	252,991,180
Number of sequences	7,851,115
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Length adjustment	15
Effective length of query	2
Effective length of database	25605224455
Effective search space	51210448910
Effective search space used	51210448910

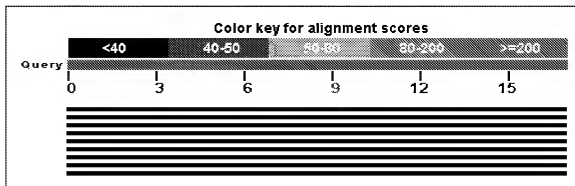
New Designing or Testing PCR Primers? Try your s

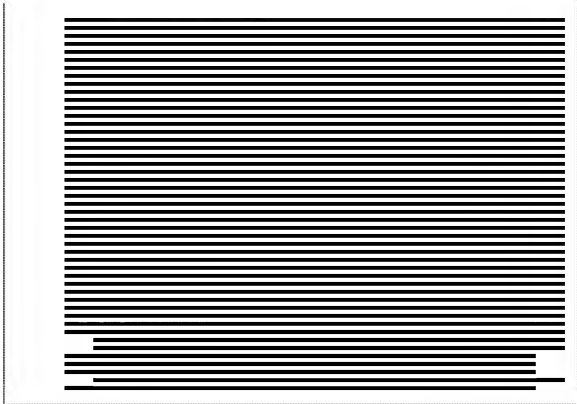
Graphic Summary

Distribution of 129 Blast Hits on the Query Sequence

?

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)



NW_002196569.1	Ralstonia solanacearum IPO1609 >emb CU914168.1 Ralstonia solanacearum strain IPO1609 Genome Draft	34.2	34.2	100%	2.6	100%	
NW_002196522.1	Ralstonia solanacearum MoIK2 >emb CU694390.1 Ralstonia solanacearum strain MoIK2 Genome Draft	34.2	34.2	100%	2.6	100%	
XM_001915641.1	PREDICTED: Equus caballus similar to Glutathione peroxidase 2 (GSHPX-2) (GPX-2) (Glutathione peroxidase- gastrointestinal) (GSHPX-GI) (LOC100146145), mRNA	34.2	34.2	100%	2.6	100%	
XM_001916096.1	PREDICTED: Equus caballus similar to glutathione peroxidase 1 (LOC100053396), mRNA	34.2	34.2	100%	2.6	100%	
CP000958.1	Burkholderia cenocepacia MC0-3 chromosome 1, complete sequence	34.2	112	100%	2.6	100%	
NW_001115119.1	Canis lupus familiaris glutathione peroxidase 1 (GPX1), mRNA	34.2	34.2	100%	2.6	100%	
XR_038530.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	34.2	34.2	100%	2.6	100%	
XR_038228.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	34.2	34.2	100%	2.6	100%	
NW_001077512.2	Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA	34.2	34.2	100%	2.6	100%	
CP000458.1	Burkholderia cenocepacia HI2424 chromosome 1, complete sequence	34.2	112	100%	2.6	100%	
AK239914.1	Sus scrofa mRNA, clone:UTR010010607, expressed in uterus	34.2	34.2	100%	2.6	100%	
AK231261.1	Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine	34.2	34.2	100%	2.6	100%	
AB121000.1	Callithrix jacchus gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%	
AB120996.1	Pan troglodytes gpx1 mRNA for glutathione peroxidase 1, complete cds	34.2	34.2	100%	2.6	100%	
CT573213.2	Frankia alni str. ACN14A chromosome, complete sequence	34.2	86.7	100%	2.6	100%	
AK225835.1	Homo sapiens mRNA for Glutathione peroxidase 1 variant, clone: FCC127C01	34.2	34.2	100%	2.6	100%	
XR_013650.1	PREDICTED: Macaca mulatta similar to Glutathione peroxidase 1 (GSHPX-1) (GPX-1) (Cellular glutathione peroxidase) (LOC706732), mRNA	34.2	34.2	100%	2.6	100%	
CP000380.1	Burkholderia cenocepacia AU 1054 chromosome 3, complete sequence	34.2	34.2	100%	2.6	100%	
AY966403.1	Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA, complete cds	34.2	34.2	100%	2.6	100%	
CP000151.1	Burkholderia sp. 383 chromosome 1, complete sequence	34.2	60.5	100%	2.6	100%	
BC007865.2	Homo sapiens glutathione peroxidase 1,	34.2	34.2	100%	2.6	100%	

[illegible]

	Placeba Cot 25-normalized of Homo sapiens (human)						
CR595371.1	full-length cDNA clone CS0DC025YE23 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	34.2	34.2	100%	2.6	100%	
AKI30160.1	Homo sapiens cDNA FLJ26650 fis, clone MPE04848, highly similar to Glutathione peroxidase (EC 1.11.1.9)	34.2	34.2	100%	2.6	100%	
AC121247.2	Homo sapiens chromosome 3 clone RP11-3B7, complete sequence	34.2	34.2	100%	2.6	100%	
AB105162.1	Macaca fuscata mRNA for cytosolic glutathione peroxidase, complete cds	34.2	34.2	100%	2.6	100%	
NM_000581.2	Homo sapiens glutathione peroxidase 1 (GPX1), transcript variant 1, mRNA	34.2	34.2	100%	2.6	100%	
NM_201397.1	Homo sapiens glutathione peroxidase 1 (GPX1), transcript variant 2, mRNA	34.2	34.2	100%	2.6	100%	
CP001111.1	Stenotrophomonas maltophilia R551-3, complete genome	32.2	32.2	94%	10	100%	
AB098194.1	Codonosiga gracilis CgPTK-f mRNA for receptor-type protein tyrosine kinase, complete cds	32.2	32.2	94%	10	100%	
CP000058.1	Pseudomonas syringae pv. phaseolicola 1448A, complete genome	32.2	32.2	94%	10	100%	
AF396866.1	Bacteriophage Mx8, complete genome	32.2	32.2	94%	10	100%	
BX950851.1	Erwinia carotovora subsp. atroseptica SCRI1043, complete genome	32.2	32.2	94%	10	100%	
AY596297.1	Haloarcula marismortui ATCC 43049 chromosome I, complete sequence	32.2	84.7	94%	10	100%	
AE015451.1	Pseudomonas putida KT2440 complete genome	32.2	32.2	94%	10	100%	
J05222.1	Halobacterium marismortui ribosomal protein gene cluster	32.2	32.2	94%	10	100%	
CP001322.1	Desulfatibacillum alkenivorans AK-01, complete genome	30.2	30.2	88%	41	100%	
AM920436.1	Penicillium chrysogenum Wisconsin 54-1255 complete genome, contig Pc00c21	30.2	84.7	94%	41	100%	
AC232899.1	Oryza officinalis clone OO_Ba011fF15, complete sequence	30.2	30.2	88%	41	100%	
AM747721.1	Burkholderia cenocepacia J2315 chromosome 2, complete genome	30.2	56.5	94%	41	100%	
CP000854.1	Mycobacterium marinum M, complete genome	30.2	56.5	88%	41	100%	
CP001026.1	Burkholderia ambifaria MC40-6 chromosome 2, complete sequence	30.2	56.5	100%	41	100%	
NW_001914855.1	Podospora anserina DSM 980 genomic scaffold chrml_SC2 >emb CU633901.1 Podospora anserina genomic DNA chromosome 1, supercontig 2	30.2	30.2	88%	41	100%	
CP000959.1	Burkholderia cenocepacia MC0-3 chromosome 2, complete sequence	30.2	30.2	88%	41	100%	
XR_017747.2	PREDICTED: Homo sapiens misc_RNA (LCNLI1), miscRNA	30.2	30.2	88%	41	100%	
EUI37666.1	Mycococcus fulvus strain l24B02 plasmid pMF1, complete sequence	30.2	30.2	88%	41	100%	

Now Designing or Testing PCR Primers? Try your s



Alignments Select All Get selected sequences Distance tree of results

>ref|NW_002196569.1|  Ralstonia solanacearum IPO1609
emb|CU914168.1|  Ralstonia solanacearum strain IPO1609 Genome Draft
Length=3372855

Features in this part of subject sequence:
glutathione peroxidase protein

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus


```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||
Sbjct 2635709 CTCGGCTTCCCGTGCAA 2635693
```

>ref|NW_002196522.1|  Ralstonia solanacearum MolK2
emb|CU694390.1|  Ralstonia solanacearum strain MolK2 Genome Draft
Length=237010

Features in this part of subject sequence:
glutathione peroxidase protein

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||
Sbjct 131900 CTCGGCTTCCCGTGCAA 131916
```

>ref|XM_001915641.1|  PREDICTED: Equus caballus similar to Glutathione peroxida
(GSHPx-2) (GPx-2) (Glutathione peroxidase-gastrointestinal)
(GSHPx-GI) (LOC100146145), mRNA
Length=573

GENE ID: 100146145 LOC100146145 | similar to Glutathione peroxidase 2 (GSHPx-2)
(GPx-2) (Glutathione peroxidase-gastrointestinal) (GSHPx-GI) [Equus caballus]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||
Sbjct 190    CTCGGCTTCCCGTGCAA 206
```

>ref|XM_001916096.1|  PREDICTED: Equus caballus similar to glutathione peroxida
(LOC100053396), mRNA

Length=606

GENE ID: 100053396 LOC100053396 | similar to glutathione peroxidase 1 [Equus caballus]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 214 CTCGGCTTCCCGTGCAA 230

>gb|CP000958.1| Burkholderia cenocepacia MC0-3 chromosome 1, complete sequence
Length=3532883

Sort alignments for this
E value Score Percen
Query start position

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 2284247 CTCGGCTTCCCGTGCAA 2284231

Features in this part of subject sequence:
short-chain dehydrogenase/reductase SDR

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 3 CGGCTTCCCGTGC 15
|||||
Sbjct 2569429 CGGCTTCCCGTGC 2569417

Features in this part of subject sequence:
conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 2872181 CTCGGCTTCCCGTGCAA 2872165

Features in this part of subject sequence:
diguanylate cyclase

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 3 CGGCTTCCCGTGC 15
|||||
Sbjct 3526443 CGGCTTCCCGTGC 3526455

>ref|NM_001115119.1| UEG Canis lupus familiaris glutathione peroxidase 1 (GPX1)
Length=838

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 235 CTCGGCTTCCCGTGCAA 251

>ref|XR_038530.1| **G** PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA
 Length=876

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1)
 (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 253 CTCGGCTTCCCGTGCAA 269

>ref|XR_038228.1| **G** PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA
 Length=878

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1)
 (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 255 CTCGGCTTCCCGTGCAA 271

>ref|NM_001077512.1| **G** Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA
 Length=613

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]
 (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 221 CTCGGCTTCCCGTGCAA 237

>gb|CP000458.1| **B** Burkholderia cenocepacia HI2424 chromosome 1, complete sequenc
 Length=3483902

Sort alignments for this
 E value Score Percen
 Query start position

Features in this part of subject sequence:
 Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 2258895 CTCGGCTTCCCGTGCAA 2258879

Features in this part of subject sequence:
short-chain dehydrogenase/reductase SDR

Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 3      CGGCTTCCCGTGC 15
           |||
Sbjct 2528844 CGGCTTCCCGTGC 2528832
```

Features in this part of subject sequence:
conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||
Sbjct 2825631 CTCGGCTTCCCGTGCAA 2825615
```

Features in this part of subject sequence:
conserved hypothetical protein


Score = 26.3 bits (13), Expect = 636
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 1      CTCGGCTTCCCGT 13
           |||
Sbjct 3438094 CTCGGCTTCCCGT 3438082
```

>dbj|AK239914.1|  Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus
Length=912

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||
Sbjct 312    CTCGGCTTCCCGTGCAA 328
```

>dbj|AK231261.1|  Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine
Length=936


Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||
Sbjct 327    CTCGGCTTCCCGTGCAA 343
```

>dbj|AB121000.1| Callithrix jacchus gp1 mRNA for glutathione peroxidase 1, comp
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


```
Query 1      CTCGGCTTCCCGTGCAA 17
           |||
Sbjct 214    CTCGGCTTCCCGTGCAA 230
```

>dbj|AB120996.1|  Pan troglodytes gpx1 mRNA for glutathione peroxidase 1, compl
 cds
 Length=606

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]
 (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 214 CTCGGCTTCCCGTGCAA 230

>emb|CT573213.2|  Frankia alni str. ACN14A chromosome, complete sequence
 Length=7497934

Sort alignments for this
 E value Score Percen
 Query start position

Features in this part of subject sequence:
 Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 1918274 CTCGGCTTCCCGTGCAA 1918290

Features flanking this part of subject sequence:
 93 bp at 5' side: Putative MarR-family transcriptional regulator
 53 bp at 3' side: Putative transcriptional regulator


Score = 26.3 bits (13), Expect = 636
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 4 GGCTTCCCGTGCA 16
 |||||
 Sbjct 641315 GGCTTCCCGTGCA 641327

Features in this part of subject sequence:
 hypothetical protein; putative Amidohydrolase domain

Score = 26.3 bits (13), Expect = 636
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 3 CGGCTTCCCGTGC 15
 |||||
 Sbjct 1575841 CGGCTTCCCGTGC 1575853


>dbj|AK225835.1|  Homo sapiens mRNA for Glutathione peroxidase 1 variant, clo
 FCC127C01
 Length=874

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||


Sbjct 223 CTCGGCTTCCCGTGCAA 239

>ref|XR_013650.1|  PREDICTED: Macaca mulatta similar to Glutathione peroxidase (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) (LOC706732), mRNA
Length=811

GENE ID: 706732 LOC706732 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Macaca mulatta]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 205 CTCGGCTTCCCGTGCAA 221

>gb|CP000380.1|  Burkholderia cenocepacia AU 1054 chromosome 3, complete sequen
Length=1196094

Features in this part of subject sequence:
Glutathione peroxidase


Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 632809 CTCGGCTTCCCGTGCAA 632825

>gb|AY966403.1| Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA
complete cds
Length=858

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 237 CTCGGCTTCCCGTGCAA 253

>gb|CP000151.1|  Burkholderia sp. 383 chromosome 1, complete sequence
Length=3694126

Sort alignments for this
E value Score Percen
Query start position

Features in this part of subject sequence:
Glutathione peroxidase

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 2403347 CTCGGCTTCCCGTGCAA 2403331

Features in this part of subject sequence:
conserved hypothetical protein

Score = 26.3 bits (13), Expect = 636
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus

```

Query 1          CTCGGCTTCCCGTGCAA 17
                |||
Sbjct 3002445    CTCGGCTTCCCGTGCAA 3002429

```

>gb|BC007865.2| **UG** Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC: IMAGE:4301275), complete cds
Length=851

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1          CTCGGCTTCCCGTGCAA 17
                |||
Sbjct 230        CTCGGCTTCCCGTGCAA 246

```

>gb|BC000742.2| **UEG** Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:3505654), complete cds
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1          CTCGGCTTCCCGTGCAA 17
                |||
Sbjct 243        CTCGGCTTCCCGTGCAA 259

```

>gb|BC070258.1| **UEG** Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:6452792), complete cds
Length=866

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1          CTCGGCTTCCCGTGCAA 17
                |||
Sbjct 236        CTCGGCTTCCCGTGCAA 252

```

>gb|AY572225.1| **UG** Canis familiaris glutathione peroxidase 1 mRNA, partial cds
Length=434

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1          CTCGGCTTCCCGTGCAA 17
                |||
Sbjct 175        CTCGGCTTCCCGTGCAA 191

```

>gb|AC135371.2| **B** Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length=25901

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 8993 CTCGGCTTCCCGTGCAA 8977

>gb|AY327818.1| **U** Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cd
 Length=4877

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 2385 CTCGGCTTCCCGTGCAA 2401

>ref|NM_214201.1| **UG** Sus scrofa glutathione peroxidase 1 (GPX1), mRNA
 gb|AF532927.1| **UG** Sus scrofa cytosolic glutathione peroxidase (GPX1) mRNA, com
 cds
 Length=803

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]
 (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 235 CTCGGCTTCCCGTGCAA 251

>dbj|AB120999.1| Cebus apella gp1 mRNA for glutathione peroxidase 1, complete
 cds
 Length=606

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 214 CTCGGCTTCCCGTGCAA 230

>dbj|AB120998.1| Hylobates lar gp1 mRNA for glutathione peroxidase 1, complete
 cds
 Length=606

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||||
 Sbjct 214 CTCGGCTTCCCGTGCAA 230

>dbj|AB120997.1| Pongo pygmaeus gp1 mRNA for glutathione peroxidase 1, complete
 cds
 Length=606

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)

Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||
 Sbjct 214 CTCGGCTTCCCGTGCAA 230

>gb|DQ333996.1| Sperophilus parryii clone SP00035 glutathione peroxidase 1 mRNA partial cds
 Length=210

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||
 Sbjct 65 CTCGGCTTCCCGTGCAA 81

>gb|M83094.1|HUMGLPEX **EG** Homo sapiens cytosolic selenium-dependent glutathione gene, complete cds, and rhoh12 gene, 3' end
 Length=4407

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||
 Sbjct 2774 CTCGGCTTCCCGTGCAA 2790

>emb|Y00483.1|HSGSHPXG **EG** Human gene for glutathione peroxidase
 Length=1733

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||
 Sbjct 687 CTCGGCTTCCCGTGCAA 703

>emb|Y00433.1|HSGSHPX **UEG** Human mRNA for glutathione peroxidase (EC 1.11.1.9.)
 Length=1134

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
 |||
 Sbjct 532 CTCGGCTTCCCGTGCAA 548

>emb|X13710.1|HSPEROXP **UEG** H.sapiens unspliced mRNA for glutathione peroxidase
 Length=1100

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
 (Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

```

Query 1 CTCGGCTTCCCGTGCAA 17
      |||
Sbjct 219 CTCGGCTTCCCGTGCAA 235

```

>emb|X13709.1|HSPEROXR **UG** Human gp1 mRNA for glutathione peroxidase
Length=819

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1 CTCGGCTTCCCGTGCAA 17
      |||
Sbjct 219 CTCGGCTTCCCGTGCAA 235

```

>ref|NM_001085444.1| **UG** Oryctolagus cuniculus glutathione peroxidase 1 (GPX1),
emb|X13837.1|OCGPO **UG** Rabbit mRNA for glutathione peroxidase (EC 1.11.1.9)
Length=760

GENE ID: 100009258 GPX1 | glutathione peroxidase 1 [Oryctolagus cuniculus]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1 CTCGGCTTCCCGTGCAA 17
      |||
Sbjct 229 CTCGGCTTCCCGTGCAA 245

```

>gb|M21304.1|HUMGLP **UEG** Human glutathione peroxidase (GPX1) mRNA, complete cds
Length=856

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1 CTCGGCTTCCCGTGCAA 17
      |||
Sbjct 255 CTCGGCTTCCCGTGCAA 271

```

>gb|U39842.1|CPU39842 Cavia porcellus glutathione peroxidase mRNA, partial cds
Length=331

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```

Query 1 CTCGGCTTCCCGTGCAA 17
      |||
Sbjct 112 CTCGGCTTCCCGTGCAA 128

```

>emb|CR626479.1| **UG** full-length cDNA clone CS0CAP001YI17 of Thymus of Homo sapi
(human)
Length=838

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)


```
Strand=Plus/Plus

Query 1      CTCGGCTTCCCGTGCAA 17
            |||
Sbjct 234    CTCGGCTTCCCGTGCAA 250
```

>emb|CR620255.1| **UG** full-length cDNA clone CS0DD004YA07 of Neuroblastoma Cot 50 of Homo sapiens (human)
Length=828

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||
Sbjct 243    CTCGGCTTCCCGTGCAA 259
```

>emb|CR614747.1| **UG** full-length cDNA clone CS0DI086YP09 of Placenta Cot 25-norm of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||
Sbjct 268    CTCGGCTTCCCGTGCAA 284
```

>emb|CR601795.1| **UG** full-length cDNA clone CS0DI068YJ17 of Placenta Cot 25-norm of Homo sapiens (human)
Length=792

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||
Sbjct 188    CTCGGCTTCCCGTGCAA 204
```

>emb|CR595371.1| **UG** full-length cDNA clone CS0DC025YE23 of Neuroblastoma Cot 25 of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

```
Query 1      CTCGGCTTCCCGTGCAA 17
            |||
Sbjct 245    CTCGGCTTCCCGTGCAA 261
```


>dbj|AK130160.1| **UG** Homo sapiens cDNA FLJ26650 fis, clone MPE04848, highly simi

to Glutathione peroxidase (EC 1.11.1.9)
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 261 CTCGGCTTCCCGTGCAA 277

>gb|AC121247.2|  Homo sapiens chromosome 3 clone RP11-3B7, complete sequence
Length=170787


Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 22842 CTCGGCTTCCCGTGCAA 22858

>dbj|AB105162.1| Macaca fuscata mRNA for cytosolic glutathione peroxidase, compl
cds
Length=606

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 214 CTCGGCTTCCCGTGCAA 230

>ref|NM_000581.2|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript
1, mRNA
Length=921

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus


Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 300 CTCGGCTTCCCGTGCAA 316

>ref|NM_201397.1|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript
2, mRNA
Length=1200

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 CTCGGCTTCCCGTGCAA 17
|||||
Sbjct 300 CTCGGCTTCCCGTGCAA 316

>gb|CP001111.1|  Stenotrophomonas maltophilia R551-3, complete genome